



4

SEQUENCE LISTING

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Taylor, Robert
Bentzien, Frauke

<120> Novel Antiangiogenic Peptide Agents and Their
Therapeutic and Diagnostic Use

<130> UCSF-018/02US

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<150> 09/076,675

<151> 1998-05-12

<150> 60/046,394

<151> 1997-05-12

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aagctatattg ccatatgggt accggccccc aagtaatggt tccggtagtt gtcgacgggtg 180
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35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
115 120 125

Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu
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Asn Glu Ile Tyr Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala
145 150 155 160

Asp Glu Glu Ser Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu
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<212> PRT

<213> Homo sapiens

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 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
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 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr
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 20 25 30
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 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
 85 90 95
 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
 100 105 110
 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
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Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro
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 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
 85 90 95
 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
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<212> PRT
<213> Homo sapiens

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Glu Glu Thr Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp
35 40 45
Ser Gln Thr Ser Phe Cys Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60
Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95
Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
100 105 110
His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125
Leu Glu Asp Gly Ser Arg Arg Thr Gly Gln Ile Leu Lys Gln Thr Tyr
130 135 140
Ser Lys Phe Asp Thr Asn Ser His Asn His Asp Ala Leu Leu Lys Asn
145 150 155 160
Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
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Phe Leu Arg Met Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 18
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<213> Homo sapiens

<400> 18

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20 25 30
Glu Glu Thr Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp
35 40 45
Ser Gln Thr Ser Phe Ser Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60
Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95
Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
100 105 110
His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
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Leu Glu Asp Gly Ser Pro Arg
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<213> Homo sapiens

<400> 19

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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
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 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Ser Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro
130

<210> 25
<211> 579
<212> DNA
<213> Homo sapiens

<400> 25
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ctgtaccagc tggcatatga cacctatcag gagtttgaag aagcctatat cctgaaggag 120
cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acaggggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcatt gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctggtgt atggcgccctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tcgcacaacg atgacgcact gctcaagaac 480
tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcattc 540
gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 26
<211> 579
<212> DNA
<213> Homo sapiens

<400> 26
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ctgtaccagc tggcatatga cacctatcag gagtttgaag aagcctatat cctgaaggag 120
cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acaggggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcatt gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctggtgt atggcgccctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tcgcacaacg atgacgcact gctcaagaac 480
tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcattc 540
gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 27

<211> 579

<212> DNA

<213> Homo sapiens

<400> 27

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gacatggtcg accgtatact gtggatagtc ctcaaacttc ttcgatata ggacttcctc 120
gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtggaaggt tgtcccactt ttgcgtcgtc tttagattgg atctcgacga ggcgtagagg 240
gacgacgagt aggtcagtac cgacctcggg cacgtcgagg agtcctcgca gaagcggttg 300
tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
ccgtaggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
ttagtcagga tgctgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
atgcccgcag agatgacgaa gtccttcctg tacctgttcc agctctgtaa ggacgcgtag 540
cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579
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<210> 28

<211> 579

<212> DNA

<213> Homo sapiens

<400> 28

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tacaaggggtt ggtaagggaa taggtccgaa aaactgttgc gatacgaggc gcgggcagcg 60
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gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtggaaggt tgtcccactt ttgcgtcgtc tttagattgg atctcgacga ggcgtagagg 240
gacgacgagt aggtcagtac cgacctcggg cacgtcgagg agtcctcgca gaagcggttg 300
tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
ccgtaggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
ttagtcagga tgctgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
atgcccgcag agatgacgaa gtccttcctg tacctgttcc agctctgtaa ggacgcgtag 540
cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579
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<210> 29

<211> 192

<212> PRT

<213> Homo sapiens

<400> 29

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Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
  1             5             10             15
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Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
          20             25             30
```

```
Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
    35             40             45
```

```
Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
    50             55             60
```

```
Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
```

65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Arg His Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr
 130 135 140
 Ser Lys Phe Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 30
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr

100 105 110
 Arg His Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg
 130 135

<210> 31
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 31
 cctgaaacca aagaaaat 18

<210> 32
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 32
 Pro Glu Thr Lys Glu Asn
 1 5

<210> 33
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleotide
 sequence coding for specific cleavage site of the
 IgA protease

<400> 33
 cctagacccc caacacct 18

<210> 34
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: specific
 cleavage site of the IgA protease

<400> 34
 Pro Arg Pro Pro Thr Pro
 1 5